



PCT10

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,178

DATE: 03/13/2002

TIME: 13:58:37

Input Set : A:\10009178.txt

Output Set: N:\CRF3\03132002\J009178.raw

3 <110> APPLICANT: OKAMOTO, Hiroshi
 5 <120> TITLE OF INVENTION: Reg-Binding Protein
 7 <130> FILE REFERENCE: 3914-4
 9 <140> CURRENT APPLICATION NUMBER: US 10/009,178
 C--> 10 <141> CURRENT FILING DATE: 2002-02-15
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP00/03764
 13 <151> PRIOR FILING DATE: 2000-06-09
 15 <150> PRIOR APPLICATION NUMBER: JP 1999-164488
 16 <151> PRIOR FILING DATE: 1999-06-10
 18 <160> NUMBER OF SEQ ID NOS: 10
 20 <170> SOFTWARE: MS Word
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1599
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Rattus norvegicus
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (168)..(1259)
 31 <400> SEQUENCE: 1
 32 tcagcgagga aaatgaaatt cccattttat ttggtgcctt gtgcagggag cacactgac 60
 34 cctctagaac cttgtgtgtg aaaaagaggt cgagttttgt caaacagact catggttatg 120
 36 gcaagtgatc cgacgtgacc agagtgggca agagccacag tgaactc atg aca ggc 176
 37 Met Thr Gly
 38 1
 40 tat acc atg ttg cgg aat ggg gga gtg ggg aac ggt ggt cag acc tgt 224
 41 Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly Gln Thr Cys
 42 5 10 15
 44 atg ctg cgc tgg tcc aac cgc atc cgg ctg acc tgg ctg agt ttc acg 272
 45 Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser Phe Thr
 46 20 25 30 35
 48 ctg ttc atc atc ctg gtc ttc ttc ccc ctc att gcc cac tat tac ctc 320
 49 Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr Tyr Leu
 50 40 45 50
 52 acc act ctg gat gag gca gat gag gcc ggc aag cgc atc ttt ggc ccc 368
 53 Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe Gly Pro
 54 55 60 65
 56 cgg gct ggc aac gag ctc tgt gag gta aag cac gtc cta gat ctt tgt 416
 57 Arg Ala Gly Asn Glu Leu Cys Glu Val Lys His Val Leu Asp Leu Cys
 58 70 75 80
 60 cgg atc cgc gag tct gtg agc gaa gag ctt cta cag cta gaa gcc aag 464
 61 Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu Ala Lys
 62 85 90 95
 64 cgg cag gag ctg aac agc gag att gcc aag cta aac ctc aag att gaa 512

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65 Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu Lys Ile Glu
66 100 105 110 115
68 gcc tgt aag aag agt ata gag aac gcc aag cag gac ctg ctg cag ctc 560
69 Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu Leu Gln Leu
70 120 125 130
72 aag aat gtc att agc cag aca gag cac tcc tac aag gag ctg atg gcc 608
73 Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu Leu Met Ala
74 135 140 145
76 cag aac cag ccc aaa ctg tca ctg ccc atc cgg ctg ctc cct gag aag 656
77 Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu Pro Glu Lys
78 150 155 160
80 gat gac gct ggc ctt cca ccc ccc aag gtc act cgg ggt tgc cgg cta 704
81 Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly Cys Arg Leu
82 165 170 175
84 cac aac tgc ttc gat tac tct cgt tgc cct ctg acg tct ggc ttt cct 752
85 His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser Gly Phe Pro
86 180 185 190 195
88 gtc ttc gtc tat gac agt gac cag ttt gcc ttt ggg agc tac ctg gac 800
89 Val Phe Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser Tyr Leu Asp
90 200 205 210
92 cct ttg gtc aag cag gct ttt cag gct aca gtg aga gcc aac gtt tat 848
93 Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala Asn Val Tyr
94 215 220 225
96 gtt aca gaa aat gca gcc atc gcc tgc ctg tat gtg gtg tta gtg gga 896
97 Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val Leu Val Gly
98 230 235 240
100 gag ata caa gag ccc gct gtg ctg cag cct gcc gac ctt gag aag cag 944
101 Glu Ile Gln Glu Pro Ala Val Leu Gln Pro Ala Asp Leu Glu Lys Gln
102 245 250 255
104 ctg cat tct ctg cca cac tgg agg aca gac gga cac aac cat gtc atc 992
105 Leu His Ser Leu Pro His Trp Arg Thr Asp Gly His Asn His Val Ile
106 260 265 270 275
108 atc aat ctg tcc cgg aag tca gac aca caa aat tta ctg tac aat gtc 1040
109 Ile Asn Leu Ser Arg Lys Ser Asp Thr Gln Asn Leu Leu Tyr Asn Val
110 280 285 290
112 agt aca ggt cgg gcc atg gtg gcc cag tct acc ttc tat gct gcc cag 1088
113 Ser Thr Gly Arg Ala Met Val Ala Gln Ser Thr Phe Tyr Ala Ala Gln
114 295 300 305
116 tac aga gct ggc ttt gac ttg gtt gtg tca cca ctt gtc cat gcc atg 1136
117 Tyr Arg Ala Gly Phe Asp Leu Val Val Ser Pro Leu Val His Ala Met
118 310 315 320
120 tct gaa ccc aac ttc atg gaa atc cca cgt gta act att ttt tca ctt 1184
121 Ser Glu Pro Asn Phe Met Glu Ile Pro Arg Val Thr Ile Phe Ser Leu
122 325 330 335
124 ggg aga ggt gag gaa gaa caa gag aag ctg ggg gtg tgg aga ggc aga 1232
125 Gly Arg Gly Glu Glu Glu Gln Glu Lys Leu Gly Val Trp Arg Gly Arg
126 340 345 350 355
128 ccc ccc cca ggc tgg ggt gct ggc ccc tagactaggg tgctgacccc 1279
129 Pro Pro Pro Gly Trp Gly Ala Gly Pro

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20050203 08:15:00

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130 360

132 tgggctgggg tgctgcgtgc tacctccac tgtgaaatcg atgggtgctca caattgtctc 1339

134 ttgtaatgta tgtgattttt ttttaaggag aaaaagaaac tatttaagat tctgaagggtg 1399

136 ctactatttt tgttgccaca ggcttttaaag aaactttctg agtgggtggg gccttgccca 1459

138 cttatctttc tctcctccaa atgaggagtt aaaaatgtta ctaaattgcc cgcacgtgta 1519

140 atccgctgaa aagaaaaaaa aaaaagaaaa aaaaaaggaa ggaaagaagg aaagaaggaa 1579

142 ggaaggaagg aaggaaagga 1599

145 <210> SEQ ID NO: 2

146 <211> LENGTH: 364

147 <212> TYPE: PRT

148 <213> ORGANISM: Rattus norvegicus

150 <400> SEQUENCE: 2

151 Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly

152 1 5 10 15

154 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu

155 20 25 30

157 Ser Phe Thr Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala His

158 35 40 45

160 Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile

161 50 55 60

163 Phe Gly Pro Arg Ala Gly Asn Glu Leu Cys Glu Val Lys His Val Leu

164 65 70 75 80

166 Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu

167 85 90 95

169 Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu

170 100 105 110

172 Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu

173 115 120 125

175 Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu

176 130 135 140

178 Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu

179 145 150 155 160

181 Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly

182 165 170 175

184 Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser

185 180 185 190

187 Gly Phe Pro Val Phe Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser

188 195 200 205

190 Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala

191 210 215 220

193 Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val

194 225 230 235 240

196 Leu Val Gly Glu Ile Gln Glu Pro Ala Val Leu Gln Pro Ala Asp Leu

197 245 250 255

199 Glu Lys Gln Leu His Ser Leu Pro His Trp Arg Thr Asp Gly His Asn

200 260 265 270

202 His Val Ile Ile Asn Leu Ser Arg Lys Ser Asp Thr Gln Asn Leu Leu

203 275 280 285

205 Tyr Asn Val Ser Thr Gly Arg Ala Met Val Ala Gln Ser Thr Phe Tyr

10009178-020502

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206 290 295 300
 208 Ala Ala Gln Tyr Arg Ala Gly Phe Asp Leu Val Val Ser Pro Leu Val
 209 305 310 315 320
 211 His Ala Met Ser Glu Pro Asn Phe Met Glu Ile Pro Arg Val Thr Ile
 212 325 330 335
 214 Phe Ser Leu Gly Arg Gly Glu Glu Glu Gln Glu Lys Leu Gly Val Trp
 215 340 345 350
 217 Arg Gly Arg Pro Pro Pro Gly Trp Gly Ala Gly Pro
 218 355 360
 221 <210> SEQ ID NO: 3
 222 <211> LENGTH: 3198
 223 <212> TYPE: DNA
 224 <213> ORGANISM: Rattus norvegicus
 226 <220> FEATURE:
 227 <221> NAME/KEY: CDS
 228 <222> LOCATION: (5)..(2761)
 230 <400> SEQUENCE: 3
 231 actc atg aca ggc tat acc atg ttg cgg aat ggg gga gtg ggg aac ggt 49
 232 Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly
 233 1 5 10 15
 235 ggt cag acc tgt atg ctg cgc tgg tcc aac cgc atc cgg ctg acc tgg 97
 236 Gly Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp
 237 20 25 30
 239 ctg agt ttc acg ctg ttc atc atc ctg gtc ttc ttc ccc ctc att gcc 145
 240 Leu Ser Phe Thr Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala
 241 35 40 45
 243 cac tat tac ctc acc act ctg gat gag gca gat gag gcc ggc aag cgc 193
 244 His Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg
 245 50 55 60
 247 atc ttt ggc ccc cgg gct ggc aac gag ctc tgt gag gta aag cac gtc 241
 248 Ile Phe Gly Pro Arg Ala Gly Asn Glu Leu Cys Glu Val Lys His Val
 249 65 70 75
 251 cta gat ctt tgt cgg atc cgc gag tct gtg agc gaa gag ctt cta cag 289
 252 Leu Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln
 253 80 85 90 95
 255 cta gaa gcc aag cgg cag gag ctg aac agc gag att gcc aag cta aac 337
 256 Leu Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn
 257 100 105 110
 259 ctc aag att gaa gcc tgt aag aag agt ata gag aac gcc aag cag gac 385
 260 Leu Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp
 261 115 120 125
 263 ctg ctg cag ctc aag aat gtc att agc cag aca gag cac tcc tac aag 433
 264 Leu Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys
 265 130 135 140
 267 gag ctg atg gcc cag aac cag ccc aaa ctg tca ctg ccc atc cgg ctg 481
 268 Glu Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu
 269 145 150 155
 271 ctc cct gag aag gat gac gct ggc ctt cca ccc ccc aag gtc act cgg 529
 272 Leu Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg

10009178.CDS

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273	160		165		170		175	
275	ggt tgc cgg cta cac aac tgc ttc gat tac tct cgt tgc cct ctg acg	577						
276	Gly Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr							
277			180		185		190	
279	tct ggc ttt cct gtc ttc gtc tat gac agt gac cag ttt gcc ttt ggg	625						
280	Ser Gly Phe Pro Val Phe Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly							
281			195		200		205	
283	agc tac ctg gac cct ttg gtc aag cag gct ttt cag gct aca gtg aga	673						
284	Ser Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg							
285			210		215		220	
287	gcc aac gtt tat gtt aca gaa aat gca gcc atc gcc tgc ctg tat gtg	721						
288	Ala Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val							
289			225		230		235	
291	gtg tta gtg gga gag ata caa gag ccc gct gtg ctg cag cct gcc gac	769						
292	Val Leu Val Gly Glu Ile Gln Glu Pro Ala Val Leu Gln Pro Ala Asp							
293	240		245		250		255	
295	ctt gag aag cag ctg cat tct ctg cca cac tgg agg aca gac gga cac	817						
296	Leu Glu Lys Gln Leu His Ser Leu Pro His Trp Arg Thr Asp Gly His							
297			260		265		270	
299	aac cat gtc atc atc aat ctg tcc cgg aag tca gac aca caa aat tta	865						
300	Asn His Val Ile Ile Asn Leu Ser Arg Lys Ser Asp Thr Gln Asn Leu							
301			275		280		285	
303	ctg tac aat gtc agt aca ggt cgg gcc atg gtg gcc cag tct acc ttc	913						
304	Leu Tyr Asn Val Ser Thr Gly Arg Ala Met Val Ala Gln Ser Thr Phe							
305			290		295		300	
307	tat gct gcc cag tac aga gct ggc ttt gac ttg gtt gtg tca cca ctt	961						
308	Tyr Ala Ala Gln Tyr Arg Ala Gly Phe Asp Leu Val Val Ser Pro Leu							
309			305		310		315	
311	gtc cat gcc atg tct gaa ccc aac ttc atg gaa atc cca ccg cag gtg	1009						
312	Val His Ala Met Ser Glu Pro Asn Phe Met Glu Ile Pro Pro Gln Val							
313	320		325		330		335	
315	cca gtt aag cgg aaa tat ctc ttc act ttc cag ggt gag aag att gag	1057						
316	Pro Val Lys Arg Lys Tyr Leu Phe Thr Phe Gln Gly Glu Lys Ile Glu							
317			340		345		350	
319	tct cta aga tct agc ctt cag gag gcc cgt tcc ttt gag gaa gaa atg	1105						
320	Ser Leu Arg Ser Ser Leu Gln Glu Ala Arg Ser Phe Glu Glu Glu Met							
321			355		360		365	
323	gag ggt gac cct ccg gcc gac tat gat gat cga atc att gcc acc ctc	1153						
324	Glu Gly Asp Pro Pro Ala Asp Tyr Asp Asp Arg Ile Ile Ala Thr Leu							
325			370		375		380	
327	aag gcc gta cag gac agc aag cta gat cag gtg ctg gta gaa ttt act	1201						
328	Lys Ala Val Gln Asp Ser Lys Leu Asp Gln Val Leu Val Glu Phe Thr							
329			385		390		395	
331	tgc aaa aac cag cca aag ccc agt ctg cct act gag tgg gca ctg tgt	1249						
332	Cys Lys Asn Gln Pro Lys Pro Ser Leu Pro Thr Glu Trp Ala Leu Cys							
333	400		405		410		415	
335	ggg gag cgg gag gac cgg cta gag tta ctg aag ctc tcc acc ttc gcc	1297						
336	Gly Glu Arg Glu Asp Arg Leu Glu Leu Leu Lys Leu Ser Thr Phe Ala							
337			420		425		430	

DATE: 03/13/2002

TIME: 13:58:38

Input Set : A:\10009178.txt

Output Set: N:\CRF3\03132002\J009178.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

[illegible]